



Db 61 FCYILNLAADLFLFSMASTLSLETQPLVNTTQKHELMKLMFAVYVGLSLTAIS 120  
121 TORCLSLVLPFWKCHPRHLSAMVCGLLMTLCLMNGLTSFCSKFLKNEDECRVDM 180  
121 TORCLSLVLPFWKCHPRHLSAMVCGLLMTLCLMNGLTSFCSKFLKNEDECRVDM 180  
181 VOALINGVLTPVMTLSLTLFWWRSSQOMRRQPRFLVAVLASVLPVLSLPLSTY 240  
181 VOALINGVLTPVMTLSLTLFWWRSSQOMRRQPRFLVAVLASVLPVLSLPLSTY 240  
241 WFLVYMLSLPEMQLCPSLSRSSVSSANPIYVLSSRRSHRPTSLGTVLQOAL 300  
241 WFLVYMLSLPEMQLCPSLSRSSVSSANPIYVLSSRRSHRPTSLGTVLQOAL 300  
301 REEPELGGERTPTVTGTMGA 321  
301 REEPELGGERTPTVTGTMGA 321

## RESULT 2

US-09-254-227A-13  
Sequence 13, Application US/09254227A  
Patent No. 6696257  
GENERAL INFORMATION:  
APPLICANT: Ahmad, Sultan  
APPLICANT: Banville, Denis  
APPLICANT: Fortin, Yves  
APPLICANT: Lembo, Paola  
APPLICANT: O'Donnell, Dajan  
APPLICANT: Shi-Hsiang, Shen  
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human  
FILE REFERENCE: 81823/268117  
CURRENT APPLICATION NUMBER: US/09/254, 227A  
CURRENT FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 13  
LENGTH: 322  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-254-227A-13

Query Match 32.8%; Score 544.5; DB 2; Length 322;  
Best Local Similarity 41.9%; Pred. No. 2, 6e-41;  
Matches 134; Conservative 56; Mismatches 105; Indels 25; Gaps 10;

QY 1 MNQTLNNSGTVESALNYSRGSTVHTAYLVLSLAFTCGCMAGNSMTWILGPRMHRNP 60  
1 MDPYVPLVGTGKLPINGRETPCYNOTLSFTVLTCTISLVGTGNAVAVMLGPMRINA 60  
QY 61 FCYILNLAADLFLFSMASTLSLETQPLVNTTQKHELMKLMFAVYVGLSLTA 118  
61 VSIYILNLAADLFLFSMASTLSLETQPLVNTTQKHELMKLMFAVYVGLSLTA 118  
Db 61 VSIYILNLAADLFLFSMASTLSLETQPLVNTTQKHELMKLMFAVYVGLSLTA 115  
QY 119 ISTORCLSLVLPFWKCHPRHLSAMVCGLLMTLCLMNGLTSFCSKFLKNEDECR- 176  
119 ISTORCLSLVLPFWKCHPRHLSAMVCGLLMTLCLMNGLTSFCSKFLKNEDECR- 176  
116 ISTORCLSLVLPFWKCHPRHLSAMVCGLLMTLCLMNGLTSFCSKFLKNEDECR- 174  
177 RUDMVOALIMVGLTVMTLSLTLFWWRSSQOMRRQPRFLVAVLASVLPVLSLPLSTY 235  
177 RUDMVOALIMVGLTVMTLSLTLFWWRSSQOMRRQPRFLVAVLASVLPVLSLPLSTY 235  
Db 175 TSDFLPVLVLI-FLCVLVCVSSLVLTILVRLCS--RKNPLRLTYTILITLVVFLGCL 230  
175 TSDFLPVLVLI-FLCVLVCVSSLVLTILVRLCS--RKNPLRLTYTILITLVVFLGCL 230  
QY 236 PLSIYVFLVYMLSLPE-----MOVLCPSLSRSSVSSANPIYVLSSRRSHRPLTR 290  
236 PLSIYVFLVYMLSLPE-----MOVLCPSLSRSSVSSANPIYVLSSRRSHRPLTR 290  
Db 231 PFGILGALYRMLNLEVLVCHYLVCMEL-----SSLNSANPIIYFPGSFR-QORNQ 285  
231 PFGILGALYRMLNLEVLVCHYLVCMEL-----SSLNSANPIIYFPGSFR-QORNQ 285  
QY 291 SLGTVLQOALREEPELGG 310  
291 SLGTVLQOALREEPELGG 310  
Db 286 NLKVLVLOALQDKPEVDKGE 305  
286 NLKVLVLOALQDKPEVDKGE 305

## RESULT 3

US-09-254-227A-11  
Sequence 11, Application US/09254227A  
Patent No. 6696257  
GENERAL INFORMATION:  
APPLICANT: Ahmad, Sultan  
APPLICANT: Banville, Denis  
APPLICANT: Fortin, Yves  
APPLICANT: Lembo, Paola  
APPLICANT: O'Donnell, Dajan  
APPLICANT: Shi-Hsiang, Shen  
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human  
FILE REFERENCE: 81823/268117  
CURRENT APPLICATION NUMBER: US/09/254, 227A  
CURRENT FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 11  
LENGTH: 322  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-254-227A-11

Query Match 32.5%; Score 539.5; DB 2; Length 322;  
Best Local Similarity 42.4%; Pred. No. 7, 5e-41;  
Matches 137; Conservative 54; Mismatches 101; Indels 31; Gaps 12;

QY 1 MNQTLNNSGTVESALNYSRGSTVHTAYLVLSLAFTCGCMAGNSMTWILGPRMHRNP 57  
1 MDPYVPLVGTGKLPIN--GRETEPCYNOTLSFTVLTCTISLVGTGNAVAVMLGCRKR 57  
Db 58 RNPFCYILNLAADLFLFSMASTLSLETQPLVNTTQKHELMKLMFAVYVGLSL 115  
58 RNPFCYILNLAADLFLFSMASTLSLETQPLVNTTQKHELMKLMFAVYVGLSL 115  
Db 58 RNPFCYILNLAADLFLFSMASTLSLETQPLVNTTQKHELMKLMFAVYVGLSL 112  
116 LTAISTORCLSLVLPFWKCHPRHLSAMVCGLLMTLCLMNGLTSFCSKFLKNEDECR- 174  
116 LTAISTORCLSLVLPFWKCHPRHLSAMVCGLLMTLCLMNGLTSFCSKFLKNEDECR- 174  
113 LTAISTORCLSLVLPFWKCHPRHLSAMVCGLLMTLCLMNGLTSFCSKFLKNEDECR- 171  
175 -CRVVMVOALIMVGLTVMTLSLTLFWWRSSQOMRRQPRFLVAVLASVLPVLI 232  
175 -CRVVMVOALIMVGLTVMTLSLTLFWWRSSQOMRRQPRFLVAVLASVLPVLI 232  
Db 172 WCETSDFLPVLVLI-FLCVLVCVSSLVLTILVRLCS--RKNPLRLTYTILITLVVFL 227  
172 WCETSDFLPVLVLI-FLCVLVCVSSLVLTILVRLCS--RKNPLRLTYTILITLVVFL 227  
QY 233 CSLPLSIYVFLVYMLSLPE-----MOVLCPSLSRSSVSSANPIYVLSSRRSHRPL 287  
233 CSLPLSIYVFLVYMLSLPE-----MOVLCPSLSRSSVSSANPIYVLSSRRSHRPL 287  
Db 228 CGPPLGILGALYRMLNLEVLVCHYLVCMEL-----SSLNSANPIIYFPGSFR-QOR 282  
228 CGPPLGILGALYRMLNLEVLVCHYLVCMEL-----SSLNSANPIIYFPGSFR-QOR 282  
QY 288 PLSIYVFLVYMLSLPE-----MOVLCPSLSRSSVSSANPIYVLSSRRSHRPL 310  
288 PLSIYVFLVYMLSLPE-----MOVLCPSLSRSSVSSANPIYVLSSRRSHRPL 310  
Db 283 NRQNLKVLVLOALQDKPEVDKGE 305  
283 NRQNLKVLVLOALQDKPEVDKGE 305

## RESULT 4

US-10-314-048A-20  
Sequence 20, Application US/10314048A  
Patent No. 6902902  
GENERAL INFORMATION:  
APPLICANT: Umetc, David J.  
APPLICANT: Chen, Kuoping  
APPLICANT: Richman, Jeremy  
APPLICANT: Connolly, Daniel  
APPLICANT: Dang, Huang T.  
APPLICANT: Choi, Bryan  
APPLICANT: Leonard, James  
APPLICANT: Hakak, Yaron  
APPLICANT: Liaw, Chen  
APPLICANT: Lowitz, Kevin P.  
APPLICANT: Behan, Dominic P.  
APPLICANT: Chalmers, Derek T.  
APPLICANT: Lerner, Michael  
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof  
FILE REFERENCE: 22,056, CIP  
CURRENT APPLICATION NUMBER: US/10/314,048A

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 11, 2006, 09:52:19 ; Search time 40 Seconds  
(without alignments)  
772.140 Million cell updates/sec

Title: US-10-509-484-4

Perfect score: 1661

Sequence: 1 MNQTLNSSGTVESALNYSRG.....EEPELGGETPTVGTNEMGA 321

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465.5	28.0	343	2	A35639
2	461	27.8	324	1	TVRTAS
3	438.5	26.4	325	1	TVHUS
4	437	26.3	324	2	TVHUS
5	402.5	24.2	378	2	A39485
6	263.5	15.9	351	1	A46525
7	257.5	15.5	353	2	C42009
8	241.5	14.5	352	1	S27357
9	240.5	14.5	350	1	A37963
10	230	13.8	371	1	UC5498
11	228	13.7	352	2	A46520
12	218.5	13.2	371	2	UC5796
13	214.5	12.9	364	2	A49542
14	208	12.5	353	2	JC2492
15	206.5	12.4	351	2	B42009
16	202.5	12.2	391	2	A41795
17	202.5	12.2	391	2	C41795
18	202.5	12.2	391	2	A39297
19	201.5	12.1	482	2	S65766
20	196	11.8	369	2	DA1795
21	195	11.7	346	2	S29248
22	193.5	11.6	369	2	UC5715
23	193	11.6	369	2	A45291
24	192	11.6	355	2	A55733
25	191.5	11.5	369	2	JC2083
26	190.5	11.4	369	2	JC5068
27	189.5	11.4	428	2	S30508
28	189	11.4	428	2	A39714
29	188.5	11.3	418	2	A46226

30	188	11.3	363	2	I57940	somatostatin recep
31	187.5	11.3	388	2	JN0605	somatostatin recep
32	187	11.3	350	2	A42009	N-formyl peptide r
33	186.5	11.2	359	2	A48921	interleukin-8 rece
34	186.5	11.2	369	2	B41795	somatostatin recep
35	185	11.1	362	2	A30341	G protein-coupled
36	183.5	11.0	346	2	UC5716	G protein-coupled
37	183	11.0	384	2	A47249	brain-specific som
38	182.5	11.0	428	2	A44021	somatostatin recep
39	179.5	10.8	355	2	J01231	interleukin-8 rece
40	179	10.8	363	2	I57955	somatostatin recep
41	179	10.8	364	2	JN0763	somatostatin recep
42	178.5	10.7	350	2	A39445	interleukin-8 rece
43	176.5	10.6	356	2	S42096	interleukin-8 rece
44	176	10.6	360	2	A53611	interleukin-8 rece
45	176	10.6	473	2	JC5835	anaphylatoxin C3a

## ALIGNMENTS

## RESULT 1

A35639  
G protein-coupled receptor R1A - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 09-Jul-2004  
C/Accession: A35639  
R/Rose, P.C.; Figler, R.A.; Corjay, M.H.; Barber, C.M.; Adam, N.; Harcus, D.R.; Lynch, K  
Proc. Natl. Acad. Sci. U.S.A. 87, 3052-3056, 1990  
A/Title: R1A, a candidate G protein-coupled receptor: cloning, sequencing, and tissue di  
A/Reference number: A35639; PMID:90222168; PMID:2109324  
A/Accession: A35639  
A/Molecule type: mRNA  
A/Residues: 1-343 <ROS>  
A/Cross-references: UNIPROT:P23749; UNIPARC:UP10000046F10; GB:M35297; NID:G206809; PIDN:  
C/Keywords: G protein-coupled receptor; glycoprotein; membrane protein  
F/4/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 28.0%; Score 465.5; DB 2; Length 343;

Best Local Similarity 35.7%; Pred. No. 7.4e-33;

Matches 121; Conservative 59; Mismatches 122; Indels 37; Gaps 11;

QY	2	NTLNSSGTVESALNYSRGSTVHTAVLVLSLA-----MFTCLCGAGNSMVI	49
DB	13	NQMKCPGSEALNYSRG-----FLTEIQIATLPPAVNTYIFLLCLCGVNGVL	66
QY	50	WLGFMRHNPFCIYILNIAADLFLPSMA--STLSLEQPLVNTDKVHELMKRLMYF	107
DB	67	WFGFSIKRTPSISYIFLHLSADGIVLPSKAVIALINMGTF-LGSPDPYRHRVRSIVGLC	125
QY	108	AYVVGSLTLTAISTQCSVLFPIMFKCHRRHLSAMVCGILMTCLMNGLTSSCSKF	167
DB	126	TFPAGVSLPLPAISIERCVSIFPMWYRRPRLSAGVALLMLLSFLVTSIHNFCC-NF	184
QY	168	L--KFNEDCFRDVQWQALINGVLPVNTLSLFLFVVRSSQOMRROPRLFFVVL	225
DB	185	LGHASGTCLAMNDISGLILFLPCPLMVLPCALILAVEGRAR--KORSKALNHVLA	243
QY	226	SVLVFLICLPISIVFWLVYLSLP---PEMQVLCSIRLSSVSSANPIYFLVGSR	282
DB	244	IYGVFLVSSIVYIGIDWFLFWFOIPAPPEY-----VTDLCICINSSAKPIVYFLAGND	297
QY	283	RSRRLPRLSLGTYLQALRE--EPELEGGETPTVGTNEM	319
DB	298	KSQRL--WEPLRVFORLRDGAEPDASSTENTVTMEM	335

## RESULT 2

transforming protein mas - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 31-Dec-1989 #sequence\_revision 31-Dec-1989 #text\_change 09-Jul-2004

C:Accession: A31816  
 R:Young, D.; O'Neill, K.; Jessell, T.; Wigler, M.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 5333-5342, 1988  
 A:Title: Characterization of the rat mas oncogene and its high-level expression in the H  
 A:Reference number: A31816; MUID:88276953; PMID:2455902  
 A:Accession: A31816  
 A:Molecule type: mRNA  
 A:Residues: 1-324 <YOU>  
 A:Cross-references: UNIPROT:P12526; UNIPARC:UPI0000043DE7; GB:J03823; NID:G205313; PIDN:  
 C:Genetics:  
 A:Gene: mas  
 C:Superfamily: mas transforming protein  
 C:Keywords: G protein-coupled receptor; transforming protein; transmembrane protein  
 F:31-47/Domain: transmembrane #status predicted <TM1>  
 F:72-88/Domain: transmembrane #status predicted <TM2>  
 F:149-165/Domain: transmembrane #status predicted <TM3>  
 F:185-204/Domain: transmembrane #status predicted <TM4>  
 F:225-243/Domain: transmembrane #status predicted <TM5>

Query Match 27.8%; Score 461; DB 1; Length 324;  
 Best Local Similarity 33.9%; Pred. No. 1.7e-32;  
 Matches 114; Conservative 64; Mismatches 118; Indels 40; Gaps 10;

OY 1 MNOTLNSGIVSALNYSRG-----TVHTAYLVLSLAFMFCCLGAGNSMVTWLGFRM 56  
 DB 1 MDSNMTSLAEKAMNTSSRNASLGSHPPIPIVHWVMSISPLGFEVNGILLMFLCFRM 60  
 OY 57 HRNPFCTIILNLAADL-----LFLFSMASTLSLE-----TQPLVNTDKVHELMKRL 104  
 DB 61 RRPFTVITHTSTADISLPCIFILSDYALDYELSSGHYITVLSVT----- 110  
 OY 105 MYFATVGLSLTALSTORCLSVLPFWKCHRPRLHSAMVCGILMTCLLMGLTSSFC 164  
 DB 111 FLFGYNTGLYLTALISVERCLSVLPYWRCHRPQHSAPFALMLALCLVTTMEYVMC 170  
 OY 165 --SKLKNEDRCFRVDVMOALIMGVLTVPWTLSSLTFLVWRRSSQWRQPTRLFVV 222  
 DB 171 IDGSEHSQSDCRVIVIFIALISFLVPLMLVSTLLVVKIRNT--WASHSKLYIV 228  
 OY 223 VLASVLPFLCPLSLPIYFVL--YMLSLPEMQVLCFSLSSSVSSANPVIYFLVG 280  
 DB 229 IMVTIITFLIFAMPKRVLYLYEYEWSTFGN-----LNHISLFTINSSANPFIYFVG 283  
 OY 281 SRRSHRLPRLSLGTYLQALREE--PELEGGETPV 314  
 DB 284 SSKKKRF-RESLKVLTTRAFKDEMQRDEGNGNTV 318

RESULT 3  
 TVHUS  
 transforming protein mas - human  
 C:Species: Homo sapiens (man)  
 C:Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #next\_change 09-Jul-2004  
 C:Accession: A01375  
 R:Young, D.; Walliches, G.; Birchmeier, C.; Faano, O.; Wigler, M.  
 Cell 45, 711-719, 1986  
 A:Title: Isolation and characterization of a new cellular oncogene encoding a protein w  
 A:Reference number: A01375; MUID:86218084; PMID:3708691  
 A:Accession: A01375  
 A:Molecule type: DNA  
 A:Residues: 1-325 <YOU>  
 A:Cross-references: UNIPROT:P04201; UNIPARC:UPI000050458; GB:M13150; NID:G187388; PIDN:  
 C:Genetics:  
 A:Gene: GDB:MAS1  
 A:Cross-references: GDB:120166; OMIM:165180  
 A:Map position: 6q24-q27  
 C:Superfamily: mas transforming protein  
 C:Keywords: G protein-coupled receptor; glycoprotein; proto-oncogene; transforming prote  
 F:31-61/Domain: transmembrane #status predicted <TM1>  
 F:66-97/Domain: transmembrane #status predicted <TM2>  
 F:105-135/Domain: transmembrane #status predicted <TM3>  
 F:150-172/Domain: transmembrane #status predicted <TM4>  
 F:186-214/Domain: transmembrane #status predicted <TM5>

F:225-250/Domain: transmembrane #status predicted <TM6>  
 F:258-286/Domain: transmembrane #status predicted <TM7>  
 F:5,16,22,27/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.4%; Score 438.5; DB 1; Length 325;  
 Best Local Similarity 33.6%; Pred. No. 1.5e-30;  
 Matches 107; Conservative 58; Mismatches 114; Indels 39; Gaps 9;

OY 7 SSGTVESALNYSRG-----STVHTAYLVLSLAFMFCCLGAGNSMVTWLGFRHRRPF 61  
 DB 7 TSFVVEEPTNISTGNASVGNHROIPIVHWVMSISPLGFEVNGILLMFLCFRRRRPF 66  
 OY 62 CIYIILNLAADL-----LFLFSMASTLSLE-----TQPLVNTDKVHELMKRLMYFAY 109  
 DB 67 TVYIITHTSLADISLPCIFILSDYALDYELSSGHYITVLSVT-----FLGXY 116  
 OY 110 TVGLSLTALSTORCLSVLPFWKCHRPRLHSAMVCGILMTCLLMGLTSSFCSEKYLK 169  
 DB 117 NGLYLTALISVERCLSVLPYWRCHRPQHSAPFALMLALCLVTTMEYVMCIDREE 176  
 OY 170 FNEDR--CFRVDVMOALIMGVLTVPWTLSSLTFLVWRRSSQWRQPTRLFVVLASV 227  
 DB 177 ESHSRNDCAVILIFIALISFLVFTPLMLVSTLLVVKIRNT--WASHSKLYIYIMVTI 234  
 OY 228 LVFLICSLPLSTYFVL--YMLSLPEMQVLCFSLSSSVSSANPVIYFLVGRSRH 285  
 DB 235 IIFLIFAMPKRVLYLYEYEWSTFGN-----LNHISLFTINSSANPFIYFVSSSKK 289  
 OY 286 RLPTSLGTYLQALREE 303  
 DB 290 RF-XESLKVLTTRAFKDE 306

RESULT 4  
 S51001  
 transforming protein mas - mouse  
 N:Alternate names: mas proto-oncogene protein; probable G protein-coupled receptor mas  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #next\_change 09-Jul-2004  
 C:Accession: S51001; 148647; S29619  
 R:Metzger, R.; Bader, M.; Ludwig, T.; Berberich, C.; Bunnemann, B.; Ganten, D.  
 FEBS Lett. 357, 27-32, 1995  
 A:Title: Expression of the mouse and rat mas proto-oncogene in the brain and peripheral  
 A:Reference number: S51001; MUID:95094925; PMID:8001672  
 A:Accession: S51001  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-324 <MET>  
 A:Cross-references: UNIPROT:P30554; UNIPARC:UPI00003B44B; EMBL:X67735  
 R:Metzger, R.; Bader, M.; Ludwig, T.; Berberich, C.; Bunnemann, B.; Ganten, D.  
 FEBS Lett. 357, 27-32, 1995  
 A:Title: Expression of the mouse and rat mas proto-oncogene in the brain and peripheral  
 A:Reference number: 148647; MUID:95094925; PMID:8001672  
 A:Accession: 148647  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-87, '1', 89-324 <RES>  
 A:Cross-references: UNIPARC:UPI0000029856; EMBL:X67735; NID:G53011; PIDN:CAA47964.1; PI  
 C:Genetics:  
 A:Gene: mas  
 C:Superfamily: mas transforming protein  
 C:Keywords: G protein-coupled receptor; proto-oncogene; transmembrane protein

Query Match 26.3%; Score 437; DB 2; Length 324;  
 Best Local Similarity 33.8%; Pred. No. 2.1e-30;  
 Matches 116; Conservative 61; Mismatches 112; Indels 54; Gaps 12;

OY 1 MNOTLNSGIVSALNYSR-----GST-----YHTAYLVLSLAFMFCCLGAGNSMVT 49  
 DB 1 MDSNMTSLAEKAMNTSSRNASLGSHPPIPIVHWVMSISPL-----GFVNGITLL 53  
 OY 50 WLQGRHNPFCIYILNLAADLFLFSMASTLSLETQPLVNTDKV--HELMKRLMY- 106

GenCore version 5.1.8  
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## OM protein - protein search, using sw model

Run on: May 11, 2006, 09:57:49 ; Search time 28 Seconds  
(without alignments)

538.235 Million cell updates/sec

Title: US-10-509-484-4

Perfect score: 1661  
1 MNQTLNNGSGVYESALNYSRSG.....EEPELGGGPTVGTNEMGA 321

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database : Published Applications AA New:

1: /SIDS5/ptodata/1/pubppaa/US08\_NEW\_PUB.pep1.\*  
2: /SIDS5/ptodata/1/pubppaa/US06\_NEW\_PUB.pep.\*  
3: /SIDS5/ptodata/1/pubppaa/US07\_NEW\_PUB.pep.\*  
4: /SIDS5/ptodata/1/pubppaa/US08\_NEW\_PUB.pep.\*  
5: /SIDS5/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep.\*  
6: /SIDS5/ptodata/1/pubppaa/US09\_NEW\_PUB.pep.\*  
7: /SIDS5/ptodata/1/pubppaa/US09\_NEW\_PUB.pep1.\*  
8: /SIDS5/ptodata/1/pubppaa/US10\_NEW\_PUB.pep1.\*  
9: /SIDS5/ptodata/1/pubppaa/US10\_NEW\_PUB.pep1.\*  
10: /SIDS5/ptodata/1/pubppaa/US11\_NEW\_PUB.pep1.\*  
11: /SIDS5/ptodata/1/pubppaa/US11\_NEW\_PUB.pep1.\*  
12: /SIDS5/ptodata/1/pubppaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1661	100.0	321	9	US-10-509-484-4
2	912.5	54.9	319	9	US-10-509-484-2
3	544.5	32.8	322	9	US-10-747-702-13
4	539.5	32.5	322	9	US-10-747-702-11
5	537.5	32.4	322	9	US-10-747-702-9
6	537	32.3	322	9	US-10-747-702-7
7	535	31.6	337	9	US-10-747-702-1
8	532	31.4	330	9	US-10-332-186-1
9	510	30.7	322	9	US-10-747-702-3
10	501	30.2	330	11	US-11-206-587-8
11	492	29.6	322	9	US-10-747-702-5
12	481.5	29.0	343	9	US-10-055-877-244
13	476.5	28.7	343	9	US-10-055-877-245
14	476.5	28.7	343	9	US-10-055-877-246
15	465.5	28.0	342	9	US-10-055-877-246
16	462.5	27.8	311	9	US-10-980-388-111
17	462.5	27.8	311	9	US-10-980-388-62
18	462	27.8	311	9	US-10-980-388-113
19	451.5	27.2	319	9	US-10-055-877-247
20	416	25.0	340	9	US-10-055-877-69
21	364	21.9	323	9	US-10-980-388-119

22	270.5	16.3	187	9	US-10-980-388-39	Sequence 39, Appl
23	270.5	16.3	187	9	US-10-980-388-98	Sequence 98, Appl
24	269.5	16.2	349	9	US-10-237-813-24	Sequence 24, Appl
25	257.5	15.5	353	9	US-10-508-765-2	Sequence 2, Appl1
26	257.5	15.5	353	9	US-10-237-813-13	Sequence 13, Appl
27	255.5	15.4	349	9	US-10-237-813-14	Sequence 14, Appl
28	254.5	15.3	349	9	US-10-237-813-15	Sequence 15, Appl
29	253.5	15.3	353	11	US-11-218-281-25	Sequence 25, Appl
30	253.5	15.3	353	11	US-11-129-107-2	Sequence 2, Appl1
31	245.5	14.8	349	9	US-10-237-813-16	Sequence 16, Appl
32	243	14.6	356	9	US-10-237-813-21	Sequence 21, Appl
33	243	14.6	356	11	US-11-218-281-27	Sequence 27, Appl
34	241.5	14.5	211	9	US-10-980-388-97	Sequence 97, Appl
35	240.5	14.5	350	9	US-10-502-145-1	Sequence 1, Appl1
36	240.5	14.5	350	9	US-10-237-813-22	Sequence 22, Appl
37	240.5	14.5	350	11	US-11-169-976-9	Sequence 9, Appl1
38	240.5	14.5	350	11	US-11-218-281-31	Sequence 31, Appl
39	239	14.4	395	9	US-10-237-813-23	Sequence 23, Appl
40	239	14.4	395	11	US-11-218-281-29	Sequence 29, Appl
41	239	14.4	395	11	US-11-296-524-2	Sequence 2, Appl1
42	239	14.4	395	11	US-11-296-524-8	Sequence 8, Appl1
43	230	13.8	371	9	US-10-237-813-5	Sequence 5, Appl1
44	230	13.8	371	11	US-11-134-811-4	Sequence 4, Appl1
45	230	13.8	371	11	US-11-218-281-2	Sequence 2, Appl1

## ALIGNMENTS

RESULT 1																												
US-10-509-484-4																												
Sequence 4, Application US/10509484																												
Publication No. US20060073516A1																												
GENERAL INFORMATION:																												
APPLICANT: Takeda Chemical Industries, Ltd.																												
TITLE OF INVENTION: Novel Screening Method																												
FILE REFERENCE: R04-117PCT																												
CURRENT APPLICATION NUMBER: US/10/509,484																												
CURRENT FILING DATE: 2004-09-27																												
PRIOR APPLICATION NUMBER: JP 2002-093045																												
PRIOR FILING DATE: 2002-03-28																												
PRIOR APPLICATION NUMBER: JP 2002-361580																												
PRIOR FILING DATE: 2002-12-13																												
NUMBER OF SEQ ID NOS: 10																												
SOFTWARE: PatentIn version 3.1																												
SEQ ID NO 4																												
LENGTH: 321																												
TYPE: PRT																												
ORGANISM: Homo sapiens																												
US-10-509-484-4																												
Query Match																												
Best Local Similarity 100.0%; Score 1661; DB 9; Length 321;																												
Best Local Similarity 100.0%; Pred. No. 1.3e-139;																												
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;																												
QY	1	MNQT	LNSG	VYES	ALNYS	RSG	STV	TAT	LV	US	SL	AM	FT	CL	CG	MA	GN	SV	W	IL	GR	M	R	N	P	60		
DB	1	MNQT	LNSG	VYES	ALNYS	RSG	STV	TAT	LV	US	SL	AM	FT	CL	CG	MA	GN	SV	W	IL	GR	M	R	N	P	60		
QY	61	FC	IT	IL	ML	AA	AD	LL	FL	FS	MA	ST	LS	LE	TP	LV	NT	DK	YH	E	L	M	K	L	M	120		
DB	61	FC	IT	IL	ML	AA	AD	LL	FL	FS	MA	ST	LS	LE	TP	LV	NT	DK	YH	E	L	M	K	L	M	120		
QY	121	T	Q	R	C	L	S	V	L	F	P	I	M	F	K	R	H	L	S	A	V	C	G	L	I	M	180	
DB	121	T	Q	R	C	L	S	V	L	F	P	I	M	F	K	R	H	L	S	A	V	C	G	L	I	M	180	
QY	181	V	O	A	L	L	I	N	G	V	L	T	P	V	T	L	S	L	T	F	V	W	R	S	S	O	Q	240
DB	181	V	O	A	L	L	I	N	G	V	L	T	P	V	T	L	S	L	T	F	V	W	R	S	S	O	Q	240
QY	241	M	F	V	L	I	N	G	V	L	T	P	V	T	L	S	L	T	F	V	W	R	S	S	O	Q	300	
DB	241	M	F	V	L	I	N	G	V	L	T	P	V	T	L	S	L	T	F	V	W	R	S	S	O	Q	300	

Db 241 WFLVWMLSPPEMOVLCPFLSLSSVSSANPVIYFLVGSRRSHRLPTRSLGTVLQAL 300  
 Qy 301 REEPLEGGETPTVTGTMGA 321  
 Db 301 REEPLEGGETPTVTGTMGA 321

## RESULT 4

US-10-509-484-2  
 ; Sequence 2, Application US/10509484  
 ; Publication No. US20060073516A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Takeda Chemical Industries, Ltd.  
 ; TITLE OF INVENTION: Novel Screening Method  
 ; FILE REFERENCE: P04-117PCT  
 ; CURRENT APPLICATION NUMBER: US/10/509,484  
 ; CURRENT FILING DATE: 2004-09-27  
 ; PRIOR APPLICATION NUMBER: JP 2002-093045  
 ; PRIOR FILING DATE: 2002-03-28  
 ; PRIOR APPLICATION NUMBER: JP 2002-361580  
 ; PRIOR FILING DATE: 2002-12-13  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 319  
 ; TYPE: PRT  
 ; ORGANISM: Rattus sp.  
 US-10-509-484-2

Query Match 54.9%; Score 912.5; DB 9; Length 319;  
 Best Local Similarity 58.5%; Pred. No. 2.4e-73;  
 Matches 190; Conservative 48; Mismatches 72; Indels 15; Gaps 6;

Qy 1 MNOTLNSG---TYESALNYSRGSSTVHTAYLVLSLAMPFCICMGANSWVILGFR- 55  
 Db 1 MNYTPYSSPAPGLTISPTMD----PTWVYFSVFLFAMATCGVIGNSVWVILSFHS 55  
 Qy 56 MHRNPFICYIINLAAADLLFLFSMASTLSTETOPLV--NTTDKVEHLMKRLMYFAYTVGL 113  
 Db 56 VORSFCTYVNLNADLLFLCMASSLSTETGPLTSTARSAYEGSKRIKRYAYTGL 115  
 Qy 114 SLTAISTORCLSVLPFWFKCHPRHLSAWVCGLLMTLCILMNGLTSSFCSEKLPKED 173  
 Db 116 SLTAISTORCLSVLPFWFKCHPRHLSAWVCGLLMTLCILMNGLTSSFCSEKLPKED 175  
 Qy 174 RCFRDMYQALIMGVLPVWTLSSLTFVWVRSSQQRROPFLFVTVLAVSLVFLIC 233  
 Db 176 QCFKDMVFNLSLIGIFMPVWVLTSAIFIRMRKNSLLQRRQPRRLYVVLITSLVFLTC 235  
 Qy 224 SLPISTIYFVLYWMLSPPEMOVLCPFLSLSSVSSANPVIYFLVGSRRSHRLPTRSLG 293  
 Db 226 SLPIGINFLYVWMLPQAVRLLYVCSRSFSSLSANPVIYFLVGSQKSHRL-QESLG 294  
 Qy 294 TVLQALREPELEGGETPTVTGNE 318  
 Db 295 AVLGRLQDER--ERETPTSTCTND 317

## RESULT 3

US-10-747-702-13  
 ; Sequence 13, Application US/10747702  
 ; Publication No. US20060068466A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ahmad, Sultan  
 ; APPLICANT: Banville, Denis  
 ; APPLICANT: Fortin, Yves  
 ; APPLICANT: Lembo, Paola  
 ; APPLICANT: O'Donnell, Dajan  
 ; APPLICANT: Shi-Hsiang, Shen  
 ; TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human  
 ; FILE REFERENCE: 81823/268117  
 ; CURRENT APPLICATION NUMBER: US/10/747,702  
 ; CURRENT FILING DATE: 2003-12-30

; PRIOR APPLICATION NUMBER: PRIO APPLICATION NUMBER: US/09/254,227  
 ; PRIOR FILING DATE: 1999-03-03  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 13  
 ; LENGTH: 322  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-747-702-13

Query Match 32.8%; Score 544.5; DB 9; Length 322;  
 Best Local Similarity 41.9%; Pred. No. 8.9e-41;  
 Matches 134; Conservative 56; Mismatches 105; Indels 25; Gaps 10;

Qy 1 MNOTLNSGTVESALNYSRGSSTVHTAYLVLSLAMPFCICMGANSWVILGFRHRRNP 60  
 Db 1 MDPTVFPVGTGLTPINGRETEPCYNOTLSFTVLTCTISLVGLTGNNAVVLGLYRRRRRA 60  
 Qy 61 FCIIYIINLAAADLLFLFSMASTLSTETOP--LVNTTDKVEHLMKRLMYFAYTVGLSLTA 118  
 Db 61 VSIYIINLAAADFLF-----SFQIRSPRLINISHLRKILVSWTEPFYGLSMLTA 115  
 Qy 119 ISTORCLSVLPFWFKCHPRHLSAWVCGLLMTLCILMNGLTSSFCSEKLPKEDR--CF 176  
 Db 116 ISTERCLSVLPFWFKCHPRHLSAWVCGLLMTLCILMNGLTSSFCSEKLPKEDR--CF 174  
 Qy 177 RVDVMOALIMGVLPVWTLSSLTFVWVRSSQQRROP--TRLFVTVLAVSLVFLICSL 235  
 Db 175 TSDPIPVWLI--FLCVLVCVSSLVFLVRLCGS--RKMPRLRYVITLITVFLVFLCGL 230  
 Qy 236 PLSTIYFVLYWMLSPPE-----MOVLCFSLSLSSVSSANPVIYFLVGSRRSHRLPTR 290  
 Db 231 PEGILGALYIRHMLNEVLYCHVLYVCMEL-----SLNSANPDIYFVGSFR--QRONRO 285  
 Qy 291 SLGTVLOALREPELEGGE 310  
 Db 286 NKLTVLORALQDKEVDKGE 305

## RESULT 4

US-10-747-702-11  
 ; Sequence 11, Application US/10747702  
 ; Publication No. US20060068466A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ahmad, Sultan  
 ; APPLICANT: Banville, Denis  
 ; APPLICANT: Fortin, Yves  
 ; APPLICANT: Lembo, Paola  
 ; APPLICANT: O'Donnell, Dajan  
 ; APPLICANT: Shi-Hsiang, Shen  
 ; TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human  
 ; FILE REFERENCE: 81823/268117  
 ; CURRENT APPLICATION NUMBER: US/10/747,702  
 ; CURRENT FILING DATE: 2003-12-30  
 ; PRIOR APPLICATION NUMBER: PRIO APPLICATION NUMBER: US/09/254,227  
 ; PRIOR FILING DATE: 1999-03-03  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 11  
 ; LENGTH: 322  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-747-702-11

Query Match 32.5%; Score 539.5; DB 9; Length 322;  
 Best Local Similarity 42.4%; Pred. No. 2.5e-40;  
 Matches 137; Conservative 54; Mismatches 101; Indels 31; Gaps 12;

Qy 1 MNOTLNSGTVESALNYSRGSSTVHTAYLVLSLAMPFC---LTCMGANSWVILGFRHRRNP 57  
 Db 1 MDPTVFPVGTGLTPIN---GRETEPCYKOTLSFTVLTCTISLVGLTGNNAVVLGLGRRMR 57  
 Qy 58 RNFPCYIINLAAADLLFLFSMASTLSTETOP--LVNTTDKVEHLMKRLMYFAYTVGLSL 115

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 11, 2006, 09:49:03 ; Search time 230 Seconds

(without alignments)  
984.672 Million cell updates/sec

Title: US-10-509-484-4

Perfect score: 1661

Sequence: 1 MNQTLNSGCTVESALNYSRG.....EPELEGGCTPTVGTNEMGA 321

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*  
2: uniprot\_crembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1661	100.0	321	1	MRGRD_HUMAN
2	1440.5	86.7	327	2	OSU9D6_MACFA
3	1439.5	86.7	320	1	MRGRD_MACFA
4	921.5	55.5	321	1	MRGRD_MOUSE
5	921.5	55.5	321	2	OSUCB4_MOUSE
6	917.5	55.2	319	1	MRGRD_RAT
7	548.5	33.0	322	1	MRGX4_HUMAN
8	544.5	32.8	322	1	SNSR5_HUMAN
9	542	32.6	322	1	SNSR3_HUMAN
10	538.5	32.4	322	1	MRGX1_HUMAN
11	538.5	32.4	322	2	Q4V9L2_HUMAN
12	538	32.4	329	2	Q4QXU5_MACMU
13	537.5	32.4	322	2	OSU9D6_MACFA
14	532	32.0	320	2	Q4QXU2_PYGRI
15	528.5	31.8	322	2	Q4QXU0_PYGRI
16	528.5	31.8	330	1	MRGX2_MACFA
17	525	31.6	323	2	Q7TN42_RAT
18	524.5	31.6	330	2	Q4QXU4_TRAFR
19	524.5	31.6	329	2	Q4QXU0_PANTR
20	522.5	31.5	329	2	Q4QXU0_PANTR
21	522	31.4	330	1	MRGX2_HUMAN
22	522	31.4	330	2	Q4QXW4_HUMAN
23	521	31.2	323	1	SNSR1_RAT
24	519	31.2	330	2	Q4QXW7_HUMAN
25	518.5	31.2	322	2	Q4QXW7_HUMAN
26	517	31.1	330	2	Q4QXW6_HUMAN
27	517	31.1	330	2	Q4QXW2_HUMAN
28	515.5	31.0	323	2	Q7TN45_RAT
29	515	31.0	330	2	Q4QXW4_HUMAN
30	515	31.0	330	2	Q4QXW7_HUMAN
31	514.5	31.0	330	2	Q4QXW3_HUMAN

32	514	30.9	321	2	Q91ZC0_MOUSE	Q91ZC0 mus musculus
33	512.5	30.9	330	2	Q4QXU0_HUMAN	Q4QXU0 homo sapien
34	511.5	30.8	320	2	Q4QXU3_PONPY	Q4QXU3 pongo pygma
35	509.5	30.7	329	2	Q4QXU6_PPRIM	Q4QXU6 pan troglod
36	508	30.6	302	1	MRGX3_MOUSE	Q91W03 mus musculus
37	506	30.5	322	1	MRGX3_HUMAN	Q91W03 mus musculus
38	503	30.3	304	1	MRGX1_MOUSE	Q91W05 mus musculus
39	500.5	30.3	331	2	Q5FVU1_RAT	Q5FVU1 mus musculus
40	499	30.0	304	1	MRGX4_RAT	Q7TN49 rattus norv
41	499	30.0	331	2	Q91YB7_RAT	Q91YB7 rattus norv
42	494.5	29.8	313	1	MRGX4_MOUSE	Q91W02 mus musculus
43	493.5	29.7	305	1	MRGX8_MOUSE	Q91ZC4 mus musculus
44	492	29.6	294	2	Q7TN48_RAT	Q7TN48 rattus norv
45	492	29.6	322	1	SNSR2_HUMAN	Q8TCD0 homo sapien

#### ALIGNMENTS

RESULT 1  
MRGRD\_HUMAN STANDARD; PRT; 321 AA.  
ID MRGRD\_HUMAN  
AC Q8TDS7; Q8NGK7;  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Mas-related G-protein coupled receptor member D (Beta-alanine receptor) (G-protein coupled receptor TGR7).  
GN Name=MRGPRD; Synonyms=MRGD;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE. PubMed=12909716; DOI=10.1073/pnas.172949100;  
RX MEDLINE=22810130; PubMed=12909716; DOI=10.1073/pnas.172949100;  
RA Zylka M.J., Dong X., Southwell A.L., Anderson D.J.;  
RT "Atypical expansion in mice of the sensory neuron-specific Mrg G protein-coupled receptor family";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048(2003).  
RN [2]  
RP NUCLEOTIDE SEQUENCE, SUBCELLULAR LOCATION, AND POSSIBLE FUNCTION.  
RC TISSUE=Liver; DOI=10.1074/jbc.M314240200;  
RX PubMed=15037633; DOI=10.1074/jbc.M314240200;  
RA Shinozaki T., Harada M., Ogi K., Maruyama M., Fujii R., Tanaka H., Fukusumi S., Komatsu H., Hosoya M., Noguchi Y., Watanabe T., Moriya T., Itoh Y., Hinuma S.;  
RT "Identification of a G protein-coupled receptor specifically responsive to beta-alanine";  
RL J. Biol. Chem. 279:23559-23564(2004).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;  
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;  
RT "Identification of G protein-coupled receptor genes from the human genome sequence";  
RL FEBS Lett. 520:97-101(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RA Suwa M., Sato T., Okouchi I., Arita M., Putani K., Matsumoto S., Tetsutani S., Aburatani H., Asai K., Akiyama Y.;  
RT "Genome-wide discovery and analysis of human seven transmembrane helix receptor genes";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: May regulate nociceptor function and/or development, including the sensation or modulation of pain. Functions as a specific membrane receptor for beta-alanine. Beta-alanine at micromolar doses specifically evoked Ca(2+) influx in cells expressing the receptor. Beta-alanine decreases forskolin-stimulated cAMP production in cells expressing the receptor, suggesting that the receptor couples with G-protein G(q) and G(i).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Localized at the

CC plasma membrane but internalized into the cytoplasm after  
 CC treatment with beta-alanine  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC Was subfamily.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL: AY427820; AAR05120.1; -; mRNA.  
 CC EMBL: AB154410; BAD20638.1; -; mRNA.  
 CC EMBL: AB083627; BAB89340.1; -; Genomic DNA.  
 CC EMBL: AB065786; BAC06005.1; ALT\_INIT; Genomic DNA.  
 CC EMBL: ENSG00000172938; Homo sapiens.  
 CC HNC; HGNC:29626; MRGPRD.  
 CC MIM: 607231; -;  
 CC InterPro: IPR000276; GPCR\_Rhodopsn.  
 CC Pfam: PF00001; Tm1.1; 1.  
 CC PRINTS: PR00237; GPCR\_Rhodopsn.  
 CC PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; FALSE\_NEG.  
 CC PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 CC G-protein coupled receptor; Glycoprotein; Receptor; Transducer;  
 KW Transmembrane.  
 FT TOPO\_DOM 1 33 Extracellular (Potential).  
 FT TRANSMEM 34 54 1 (Potential).  
 FT TOPO\_DOM 55 59 Cytoplasmic (Potential).  
 FT TRANSMEM 60 80 2 (Potential).  
 FT TOPO\_DOM 81 112 Extracellular (Potential).  
 FT TRANSMEM 113 133 3 (Potential).  
 FT TOPO\_DOM 134 142 Cytoplasmic (Potential).  
 FT TRANSMEM 143 163 4 (Potential).  
 FT TOPO\_DOM 164 184 Extracellular (Potential).  
 FT TRANSMEM 185 205 5 (Potential).  
 FT TOPO\_DOM 206 218 Cytoplasmic (Potential).  
 FT TRANSMEM 219 239 6 (Potential).  
 FT TOPO\_DOM 240 257 Extracellular (Potential).  
 FT TRANSMEM 258 280 7 (Potential).  
 FT TOPO\_DOM 281 321 Cytoplasmic (Potential).  
 FT CARBOHYD 2 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 6 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 16 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 92 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 321 AA; 36118 MW; B45AB7FB2154B40 CRC64;  
 Query Match 100.0%; Score 1661; DB 1; Length 321;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-120;  
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2  
 ID Q5U9D8\_MACFA PRELIMINARY; PRT; 337 AA.  
 AC Q5U9D8;  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Mac-related protein D.  
 GN Name=MgD;  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopithecoidea; Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Zhang L., Taylor N., Ford R., Johnson J., Paulsen J.E., Bates B.;  
 RT "Cloning and Expression of MRG Receptors in Macaque, Mouse, and  
 RT Human."  
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 DR EMBL: AY772459; AA049126.1; -; Genomic DNA.  
 DR GO: GO:0016021; C:integral to membrane; IEA.  
 DR GO: GO:0004872; F:receptor activity; IEA.  
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO: GO:0007186; P:G-protein coupled receptor protein signaling; IEA.  
 DR GO: GO:0007165; P:signal transduction; IEA.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; Tm1.1; 1.  
 DR PRINTS: PR00237; GPCR\_Rhodopsn.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.  
 SQ SEQUENCE 337 AA; 37776 MW; D41CDBA565EABE5 CRC64;  
 Query Match 86.7%; Score 1440.5; DB 2; Length 337;  
 Best Local Similarity 88.2%; Pred. No. 7.6e-103;  
 Matches 283; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

QY 1 MNQTLNNGSGTVESALNYSRGSTVHTAYLVLSLAFMTCICGMAGNSMVTWILGFRMRNP 60  
 DB 1 MNQTLNNGSGTVESALNYSRGSTVHTAYLVLSLAFMTCICGMAGNSMVTWILGFRMRNP 60  
 QY 61 FCITYILNLAADLLFESMASTLSLETOPLVNTTDKVEHLMKRLMFAVTVGLSLTAIS 120  
 DB 61 FCITYILNLAADLLFESMASTLSLETOPLVNTTDKVEHLMKRLMFAVTVGLSLTAIS 120  
 QY 121 TORCLSVLPFWFKCHRPRLHSAMVCGILMTCLINMGILTSFCSKFLKFNEDRCFRVDM 180  
 DB 121 TORCLSVLPFWFKCHRPRLHSAMVCGILMTCLINMGILTSFCSKFLKFNEDRCFRVDM 180  
 QY 181 VOALINGVLPVNTLSLTLFVWRSSSQMRROPRLFVVVLASVLFICSLPLSTY 240  
 DB 181 VOALINGVLPVNTLSLTLFVWRSSSQMRROPRLFVVVLASVLFICSLPLSTY 240  
 QY 241 WFLVYWLSTLPEPMOVLCEFSLSRLSSSVSSANPVYIFVGSRRSHRLPRTSLGTVLQOAL 300  
 DB 241 WFLVYWLSTLPEPMOVLCEFSLSRLSSSVSSANPVYIFVGSRRSHRLPRTSLGTVLQOAL 300  
 QY 301 REEPLEGGETPTVTGNEMGA 321  
 DB 301 REEPLEGGETPTVTGNEMGA 321

RESULT 3  
 MGRD MACFA STANDARD; PRT; 320 AA.  
 ID MGRD MACFA  
 AC 06L786;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Mac-related G-protein coupled receptor member D (Beta-alanine